SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Massachusetts Institute of Technology
(ii) TITLE OF INVENTION: Class BI and CI Scavenger Receptors
(iii) NUMBER OF SEQUENCES: 8
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: 2800 One Atlantic Center
1201 West Peachtree Street
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: USA
(F) ZIP: 30309-3450
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Pabst, Patrea L.
(B) REGISTRATION NUMBER: 31,284
(C) REFERENCE/DOCKET NUMBER: MIT6620
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (404) 873-8794
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(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Ashkenas, et al.
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 34
(F) PAGES: 983-1000
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 20
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATGAAGAAC TGCTTAGTTT 20

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Ashkenas, et al.
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 34
(F) PAGES: 983-1000
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 18
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATCAAGGAA TTTAACTG 18

(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 156..1683
(D) OTHER INFORMATION: /function= "Nucleotides 156 through 1683 encode the amino acid sequence for the Hamster Scavenger Receptor Class B-I."
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCACCTGCA GGGCTACTGC TGCTCCGGCC ACTGCCTGAG ACTCACCTTG CTGGAACGTG 60

AGCCTCGGCT TCTGTCATCT CTGTGGCCTC TGTCGCTTCT GTCGCTGTCC CCCTTCAGTC 120

CCTGAGCCCC GCGAGCCCGG GCCGCACACG CGGACATGGG CGGCAGCGCC AGGGCGCGCT 180

GGGTGGCGGT GGGGCTGGGC GTCGTGGGGC TGCTGTGCGC TGTGCTCGGT GTGGTTATGA 240

TCCTCGTGAT GCCCTCGCTC ATCAAACAGC AGGTACTGAA GAATGTCCGC ATAGACCCCA 300

GCAGCCTGTC CTTTGCAATG TGGAAGGAGA TCCCTGTACC CTTCTACTTG TCCGTCTACT 360

TCTTCGAGGT GGTCAATCCC AGCGAGATCC TAAAGGGTGA GAAGCCAGTA GTGCGGGAGC 420

GTGGACCCTA TGTCTACAGG GAATTCAGAC ATAAGGCCAA CATCACCTTC AATGACAATG 480

ATACTGTGTC CTTTGTGGAG CACCGCAGCC TCCATTTCCA GCCGGACAGG TCCCACGGCT 540

CTGAGAGTGA CTACATTATA CTGCCTAACA TTCTGGTCTT GGGGGGCGCA GTAATGATGG 600

AGAGCAAGTC TGCAGGCCTG AAGCTGATGA TGACCTTGGG GCTGGCCACC TTGGGCCAGC 660

GTGCCTTTAT GAACCGAACA GTTGGTGAGA TCCTGTGGGG CTATGAGGAT CCCTTCGTGA 720

ATTTTATCAA CAAATACTTA CCAGACATGT TCCCCATCAA GGGCAAGTTC GGCCTGTTTG 780

TTGAGATGAA CAACTCAGAC TCTGGGCTCT TCACTGTGTT CACGGGCGTC CAGAACTTCA 840

GCAAGATCCA CCTGGTGGAC AGATGGAATG GGCTCAGCAA GGTCAACTAC TGGCATTCAG 900

AGCAGTGCAA CATGATCAAT GGCACTTCCG GGCAGATGTG GGCACCATTC ATGACACCCC 960

AGTCCTCGCT GGAATTCTTC AGTCCGGAAG CCTGCAGGTC TATGAAGCTC ACCTACCATG 1020

ATTCAGGGGT GTTTGAAGGC ATCCCCACCT ATCGCTTCAC AGCCCCTAAA ACTTTGTTTG 1080

CCAATGGGTC TGTTTACCCA CCCAATGAAG GTTTCTGCCC GTGCCTTGAA TCCGGCATTC 1140

AAAATGTCAG CACTTGCAGG TTTGGTGCAC CCCTGTTTCT GTCACACCCT CACTTCTACA 1200

ATGCAGACCC TGTGCTATCA GAAGCCGTTC TGGGTCTGAA CCCTGACCCA AGGGAGCATT 1260

CTTTGTTCCT TGACATCCAT CCGGTCACTG GGATCCCCAT GAACTGTTCT GTGAAGTTGC 1320

AGATAAGCCT CTACATCAAA GCTGTCAAGG GCATTGGGCA AACAGGGAAG ATCGAGCCCG 1380

TGGTCCTCCC ATTGCTGTGG TTTGAGCAGA GCGGTGCCAT GGGCGGCGAG CCCCTGAACA 1440

CGTTCTACAC GCAGCTGGTG CTGATGCCCC AGGTACTTCA GTATGTGCAG TATGTGCTGC 1500

TGGGGCTGGG CGGCCTCCTG CTGCTGGTGC CCGTCATCTA CCAGTTGCGC AGCCAGGAGA 1560

AATGCTTTTT ATTTTGGAGT GGTAGTAAAA AGGGCTCGCA GGATAAGGAG GCCATTCAGG 1620

CCTACTCTGA GTCTCTGATG TCACCAGCTG CCAAGGGCAC GGTGCTGCAA GAAGCCAAGC 1680

TGTAGGGTCC CAAAGACACC ACGAGCCCCC CCAACCTGAT AGCTTGGTCA GACCAGCCAT 1740

CCAGCCCCTA CACCCCGCTT CTTGAGGACT CTCTCAGCGG ACAGTCGC 1788

(2) INFORMATION FOR SEQ ID NO:4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..509
(D) OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger Receptor Class B-I."
(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 9..32
(D) OTHER INFORMATION: /note= "Putative transmembrane domain."
(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 440..464
(D) OTHER INFORMATION: /note= "Putative transmembrane domain."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..385
(D) OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent potential N-linked glycosylation sites."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21..470
(D) OTHER INFORMATION: /note= "The cysteines at positions 21, 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide linkages."
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Gly Ser Ala Arg Ala Arg Trp Val Ala Val Gly Leu Gly Val
1 5 10 15

Val Gly Leu Leu Cys Ala Val Leu Gly Val Val Met Ile Leu Val Met
20 25 30

Pro Ser Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro
35 40 45

Ser Ser Leu Ser Phe Ala Met Trp Lys Glu Ile Pro Val Pro Phe Tyr
50 55 60

Leu Ser Val Tyr Phe Phe Glu Val Val Asn Pro Ser Glu Ile Leu Lys
65 70 75 80

Gly Glu Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu
85 90 95

Phe Arg His Lys Ala Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser
100 105 110

Phe Val Glu His Arg Ser Leu His Phe Gln Pro Asp Arg Ser His Gly
115 120 125

Ser Glu Ser Asp Tyr Ile Ile Leu Pro Asn Ile Leu Val Leu Gly Gly
130 135 140

Ala Val Met Met Glu Ser Lys Ser Ala Gly Leu Lys Leu Met Met Thr
145 150 155 160

Leu Gly Leu Ala Thr Leu Gly Gln Arg Ala Phe Met Asn Arg Thr Val
165 170 175

Gly Glu Ile Leu Trp Gly Tyr Glu Asp Pro Phe Val Asn Phe Ile Asn
180 185 190

Lys Tyr Leu Pro Asp Met Phe Pro Ile Lys Gly Lys Phe Gly Leu Phe
195 200 205

Val Glu Met Asn Asn Ser Asp Ser Gly Leu Phe Thr Val Phe Thr Gly
210 215 220

Val Gln Asn Phe Ser Lys Ile His Leu Val Asp Arg Trp Asn Gly Leu
225 230 235 240

Ser Lys Val Asn Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly
245 250 255

Thr Ser Gly Gln Met Trp Ala Pro Phe Met Thr Pro Gln Ser Ser Leu
260 265 270

Glu Phe Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr His
275 280 285

Asp Ser Gly Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro
290 295 300

Lys Thr Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe
305 310 315 320

Cys Pro Cys Leu Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe
325 330 335

Gly Ala Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro
340 345 350

Val Leu Ser Glu Ala Val Leu Gly Leu Asn Pro Asp Pro Arg Glu His
355 360 365

Ser Leu Phe Leu Asp Ile His Pro Val Thr Gly Ile Pro Met Asn Cys
370 375 380

Ser Val Lys Leu Gln Ile Ser Leu Tyr Ile Lys Ala Val Lys Gly Ile
385 390 395 400

Gly Gln Thr Gly Lys Ile Glu Pro Val Val Leu Pro Leu Leu Trp Phe
405 410 415

Glu Gln Ser Gly Ala Met Gly Gly Glu Pro Leu Asn Thr Phe Tyr Thr
420 425 430

Gln Leu Val Leu Met Pro Gln Val Leu Gln Tyr Val Gln Tyr Val Leu
435 440 445

Leu Gly Leu Gly Gly Leu Leu Leu Leu Val Pro Val Ile Tyr Gln Leu
450 455 460

Arg Ser Gln Glu Lys Cys Phe Leu Phe Trp Ser Gly Ser Lys Lys Gly
465 470 475 480

Ser Gln Asp Lys Glu Ala Ile Gln Ala Tyr Ser Glu Ser Leu Met Ser
485 490 495

Pro Ala Ala Lys Gly Thr Val Leu Gln Glu Ala Lys Leu

500 505

(2) INFORMATION FOR SEQ ID NO:5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2032 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(ix) FEATURE:
(A) NAME/KEY: misc. feature
(B) LOCATION: 40..1926
(D) OTHER INFORMATION: /Function = "Nucleotides 40 through 1926 encode the amino acid sequence for the Drosophila Melanogaster Scavenger Receptor Class CI."
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACCGTATCT ATACATTAAG TTCGTAATAT CTCTGCGGAA TGGAATTTTT CTGGACTCTG 60

GCTGTGATTG TGATATATTG TATAGGTCAC ATTCATGGAC GATGTGAAAG ATCTATAGAT 120

TTGGATAATG GAAGTATAAA TTATCGACAG AGAAATATAG TGAGATTCAG ATGCAATCGC 180

GGCTACACTT TGCAGGGAAC AGTAATGCAA ACTTGCGATC GAGATGGTCG CCTTCGAGGC 240

GAAAAACCAT TCTGTGCCAG TAGGGGATGT GCGAGGCCCG AGGATCCGGA GAACGGACAC 300

GTCGAAAATC TTTCCCTAAG GGCGGATGTC GTGTGCCACG ATGGCTATGT CTTGGTCGGT 360

GGTCGCACTG CCTACTGCGA TGGAGAAAGA TGGAGCACCC AGCTGGGATC GTGTCGAAGG 420

AGCAACCACA CAAGAGATCA TTCTTGCGAT TTCGAGAGCG AGGATCAGTG CGGTTGGGAG 480

GCGGAGACAA CCTTCCGACG ACCCTGGAAG CGAGTCAGCA CGGTATCCGA TATTCACTCC 540

CTAAGAACGG GACCCCGCCA CGATCACACG TTTAAAAACG AATCCGGTGG TCATTACATG 600

CGCATGGAAA CCCAAATGGG GGCTTATGGA AGCTACCATC TGCTATCGCC GATCTATCCC 660

AGATCCCTCA CCCTGAAGAC CGCCTGCTGC TTTCGATTCC ACTACTTCAT GTTTGGCGCT 720

GGTGTGGATA ATCTGGTGGT GTCCGTTAAA CCCGTTTCGA TGCCAATGGC AACCATGTGG 780

AATAGGTTCA GAGCCAATTG CAGCAAATTT GAGATATCTG GTCAGCAGGG AACCCAGTGG 840

CTAGAGCACA CGATCAGCAT TGACGAGATG CAAGAGGACT TCCAGGTGAT ATTCACGGCA 900

ACGGATGCAA GATCCCAATT CGGAGATATT GCCATCGATG ATGTAAAGCT AATGACAGGC 960

AGTGAGTGTG GCACAAACGG ATTTAGCACC ACCACAGAAC CAACGGCTCC GACAGGCAGC 1020

AACGAGCAAC CACTGGTCTA CGATATGATA AGTTGTTCAG GTCGATGCGG AACATCAATG 1080

TCGGCCTCCA ATATAACCAA CAATGGTATA GTCATGGGAT GTGGATGTAA TGACGAGTGC 1140

CTTTCGGATG AGACTTGTTG CCTAAACTAT TTGGAGGAGT GCACAAAGGA GCTGCTCACC 1200

ACGACCGAGG ATGATATTAG TTCCCTGCCC CCAACGGTCA CATCAACAAG CACAAGCACT 1260

ACGAGGAAGT CAACAACAAC AACAACCACA AGCACGACTA CTACAAGTAC AACAACAACT 1320

AAAAGGCCAA CCACAACCAC AACAACAACA AAGGCCACAA CTACAAAGCG AACAACAACC 1380

ACTAAAAAAC CGACAACAAC TTCAACAACG CCGAAGCCAA CAACAACGAC TTCAACCACA 1440

CCAAAGTCTA CAACTTCTAC AACGTCTACA ACTTCAACAA CACCAACGAC AACAACTACA 1500

ATAAATGTGT TTACAACAAA GAAAACAACA ATAATGATCC CTACTTCCAG TACCGAAAAG 1560

ACTACAGGCA TCATCACCAC CATGAAGACA CGCAAGCGCA TCACTTGGAA CGTTGATCCT 1620

CAGGACATCG AGGGTCACAT GGACACGAGC GGAAGTACCC CCAATCCAGC TTTAGTAGTA 1680

CTTTACCTGC TACTCGGCAT TGTTCTGGTG GTAGTTCTGG CCAACGTCGT TAATCGCTGG 1740

ATAATACCAA TCACTGGATC AAAGACCAGC AGCGAAAAGG CTGTGAGATT CAAGAAGGCA 1800

TTCGATAGTC TGAAGAAGCA ACGGAAAAGA AACAGCATGG ATGATCAGCC GTTATGCGAC 1860

TCCGATAACG ACGATGTAGA GTATTTCGAA GAAATGGGCG TGGACATACG ACATAGGACC 1920

GATCTATGAG GGTAATCCCC AGTGATACCA AAACAAACGC TTAGGCCTGT GCCTATTGTA 1980

TAGGATGTTT CTAAATGTGT ATGCAAGAAT CGAATAAAAG AAAATATGCA AC 2032

(2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 629 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal
(ix) FEATURE:
(A) NAME/KEY: misc. feature
(B) LOCATION: 1..629
(D) OTHER INFORMATION: /Function = "Amino acid sequence for the Drosophila Melanogaster Scavenger Receptor Class CI."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30..353
(D) OTHER INFORMATION: /note= "Positions 30-32, 90-92, 129-131, 180-182, 253-255 and 351-353 represent potential N-glycosylation sites."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "Amino acids 1-20 represent a putative signal sequence."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21..74
(D) OTHER INFORMATION: /note= "Amino acids 21-74 represent complement control protein domain number 1."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 75..127
(D) OTHER INFORMATION: /note= "Amino acids 75-127 represent complement control protein domain number 2."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 128..312
(D) OTHER INFORMATION: /note= "Amino acids 128-312 represent an MAM domain."
(ix) FEATURE:
(A) NAME/KEY: Disulfide-bond
(B) LOCATION: 22..381
(D) OTHER INFORMATION: /note= "The cysteines at positions 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216, 217, 254, 310, 339, 343, 361, 363, 367, 373, 374 and 381 represent potential disulfide linkages."
(ix) FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 338..381
(D) OTHER INFORMATION: /note= "Amino acids 338-381 represent a somatomedin B domain."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 387..514
(D) OTHER INFORMATION: /note= "Amino acids 387-514 represent a mucin-like potential O-linked glycosylation region."

(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 544..564
(D) OTHER INFORMATION: /note= "Amino acids 544-565 represent a putative TM domain."

(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 565..629
(D) OTHER INFORMATION: /note= "Amino acids 565-629 represent a putative cytoplasmic domain."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 576..602
(D) OTHER INFORMATION: /note= "Amino acids 576-579 and 599-602 represent casein kinase II sites."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 578..592
(D) OTHER INFORMATION: /note= "Amino acids 578-580 and 590-592 represent protein kinase C sites."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 596..599
(D) OTHER INFORMATION: /note= "Amino acids 596-599 represent a cAMP protein kinase site."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Glu Phe Phe Trp Thr Leu Ala Val Ile Val Ile Tyr Cys Ile Gly
1               5                  10                  15

His Ile His Gly Arg Cys Glu Arg Ser Ile Asp Leu Asp Asn Gly Ser
            20                  25                  30

Ile Asn Tyr Arg Gln Arg Asn Ile Val Arg Phe Arg Cys Asn Arg Gly
        35                  40                  45

Tyr Thr Leu Gln Gly Thr Val Met Gln Thr Cys Asp Arg Asp Gly Arg
    50                  55                  60

Leu Arg Gly Glu Lys Pro Phe Cys Ala Ser Arg Gly Cys Ala Arg Pro
65                  70                  75                  80

Glu Asp Pro Glu Asn Gly His Val Glu Asn Leu Ser Leu Arg Ala Asp
                85                  90                  95

Val Val Cys His Asp Gly Tyr Val Leu Val Gly Gly Arg Thr Ala Tyr
            100                 105                 110

Cys Asp Gly Glu Arg Trp Ser Thr Gln Leu Gly Ser Cys Arg Arg Ser
        115                 120                 125

Asn His Thr Arg Asp His Ser Cys Asp Phe Glu Ser Glu Asp Gln Cys
    130                 135                 140

Gly Trp Glu Ala Glu Thr Thr Phe Arg Arg Pro Trp Lys Arg Val Ser
145                 150                 155                 160

Thr Val Ser Asp Ile His Ser Leu Arg Thr Gly Pro Arg His Asp His
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165 170 175

Thr Phe Lys Asn Glu Ser Gly Gly His Tyr Met Arg Met Glu Thr Gln
180 185 190

Met Gly Ala Tyr Gly Ser Tyr His Leu Leu Ser Pro Ile Tyr Pro Arg
195 200 205

Ser Leu Thr Leu Lys Thr Ala Cys Cys Phe Arg Phe His Tyr Phe Met
210 215 220

Phe Gly Ala Gly Val Asp Asn Leu Val Val Ser Val Lys Pro Val Ser
225 230 235 240

Met Pro Met Ala Thr Met Trp Asn Arg Phe Arg Ala Asn Cys Ser Lys
245 250 255

Phe Glu Ile Ser Gly Gln Gln Gly Thr Gln Trp Leu Glu His Thr Ile
260 265 270

Ser Ile Asp Glu Met Gln Glu Asp Phe Gln Val Ile Phe Thr Ala Thr
275 280 285

Asp Ala Arg Ser Gln Phe Gly Asp Ile Ala Ile Asp Asp Val Lys Leu
290 295 300

Met Thr Gly Ser Glu Cys Gly Thr Asn Gly Phe Ser Thr Thr Thr Glu
305 310 315 320

Pro Thr Ala Pro Thr Gly Ser Asn Glu Gln Pro Leu Val Tyr Asp Met
325 330 335

Ile Ser Cys Ser Gly Arg Cys Gly Thr Ser Met Ser Ala Ser Asn Ile
340 345 350

Thr Asn Asn Gly Ile Val Met Gly Cys Gly Cys Asn Asp Glu Cys Leu
355 360 365

Ser Asp Glu Thr Cys Cys Leu Asn Tyr Leu Glu Glu Cys Thr Lys Glu
370 375 380

Leu Leu Thr Thr Thr Glu Asp Asp Ile Ser Ser Leu Pro Pro Thr Val
385 390 395 400

Thr Ser Thr Ser Thr Ser Thr Thr Arg Lys Ser Thr Thr Thr Thr Thr
405 410 415

Thr Ser Thr Thr Thr Thr Ser Thr Thr Thr Thr Lys Arg Pro Thr Thr
420 425 430

Thr Thr Thr Thr Thr Lys Ala Thr Thr Thr Lys Arg Thr Thr Thr Thr
435 440 445

Lys Lys Pro Thr Thr Thr Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr
450 455 460

Ser Thr Thr Pro Lys Ser Thr Thr Ser Thr Thr Ser Thr Thr Ser Thr
465 470 475 480

Thr Pro Thr Thr Thr Thr Thr Ile Asn Val Phe Thr Thr Lys Lys Thr
485 490 495

Thr Ile Met Ile Pro Thr Ser Ser Thr Glu Lys Thr Thr Gly Ile Ile
500 505 510

Thr Thr Met Lys Thr Arg Lys Arg Ile Thr Trp Asn Val Asp Pro Gln
515 520 525

```
Asp Ile Glu Gly His Met Asp Thr Ser Gly Ser Thr Pro Asn Pro Ala
530                 535                 540

Leu Val Val Leu Tyr Leu Leu Leu Gly Ile Val Leu Val Val Val Leu
545                 550                 555                 560

Ala Asn Val Val Asn Arg Trp Ile Ile Pro Ile Thr Gly Ser Lys Thr
                565                 570                 575

Ser Ser Glu Lys Ala Val Arg Phe Lys Lys Ala Phe Asp Ser Leu Lys
            580                 585                 590

Lys Gln Arg Lys Arg Asn Ser Met Asp Asp Gln Pro Leu Cys Asp Ser
        595                 600                 605

Asp Asn Asp Asp Val Glu Tyr Phe Glu Glu Met Gly Val Asp Ile Arg
610                 615                 620

His Arg Thr Asp Leu
625
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 51..1577
(D) OTHER INFORMATION: /Function = "Nucleotides 51 through 1577 encode the amino acid sequence for the murine Scavenger Receptor Class BI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
CCGTCTCCTT CAGGTCCTGA GCCCCGAGAG CCCCTTCCGC GCACGCGGAC ATG GGC        56
                                                          Met Gly
                                                            1

GGC AGC TCC AGG GCG CGC TGG GTG GCC TTG GGG TTG GGC GCC CTG GGG      104
Gly Ser Ser Arg Ala Arg Trp Val Ala Leu Gly Leu Gly Ala Leu Gly
          5                  10                  15

CTG CTG TTT GCT GCG CTC GGC GTT GTC ATG ATC CTC ATG GTG CCC TCC      152
Leu Leu Phe Ala Ala Leu Gly Val Val Met Ile Leu Met Val Pro Ser
     20                  25                  30

CTC ATC AAG CAG CAG GTG CTC AAG AAT GTC CGC ATA GAC CCG AGC AGC      200
Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro Ser Ser
 35                  40                  45                  50

CTG TCC TTC GGG ATG TGG AAG GAG ATC CCC GTC CCT TTC TAC TTG TCT      248
Leu Ser Phe Gly Met Trp Lys Glu Ile Pro Val Pro Phe Tyr Leu Ser
                 55                  60                  65

GTC TAC TTC TTC GAA GTG GTC AAC CCA AAC GAG GTC CTC AAC GGC CAG      296
Val Tyr Phe Phe Glu Val Val Asn Pro Asn Glu Val Leu Asn Gly Gln
             70                  75                  80

AAG CCA GTA GTC CGG GAG CGT GGA CCC TAT GTC TAC AGG GAG TTC AGA      344
Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu Phe Arg
          85                  90                  95

CAA AAG GTC AAC ATC ACC TTC AAT GAC AAC GAC ACC GTG TCC TTC GTG      392
Gln Lys Val Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser Phe Val
    100                 105                 110
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GAG AAC CGC AGC CTC CAT TTC CAG CCT GAC AAG TCG CAT GGC TCA GAG      440
Glu Asn Arg Ser Leu His Phe Gln Pro Asp Lys Ser His Gly Ser Glu
115                 120                 125                 130

AGT GAC TAC ATT GTA CTG CCT AAC ATC TTG GTC CTG GGG GGC TCG ATA      488
Ser Asp Tyr Ile Val Leu Pro Asn Ile Leu Val Leu Gly Gly Ser Ile
                135                 140                 145

TTG ATG GAG AGC AAG CCT GTG AGC CTG AAG CTG ATG ATG ACC TTG GCG      536
Leu Met Glu Ser Lys Pro Val Ser Leu Lys Leu Met Met Thr Leu Ala
            150                 155                 160

CTG GTC ACC ATG GGC CAG CGT GCT TTT ATG AAC CGC ACA GTT GGT GAG      584
Leu Val Thr Met Gly Gln Arg Ala Phe Met Asn Arg Thr Val Gly Glu
        165                 170                 175

ATC CTG TGG GGC TAT GAC GAT CCC TTC GTG CAT TTT CTC AAC ACG TAC      632
Ile Leu Trp Gly Tyr Asp Asp Pro Phe Val His Phe Leu Asn Thr Tyr
    180                 185                 190

CTC CCA GAC ATG CTT CCC ATA AAG GGC AAA TTT GGC CTG TTT GTT GGG      680
Leu Pro Asp Met Leu Pro Ile Lys Gly Lys Phe Gly Leu Phe Val Gly
195                 200                 205                 210

ATG AAC AAC TCG AAT TCT GGG GTC TTC ACT GTC TTC ACG GGC GTC CAG      728
Met Asn Asn Ser Asn Ser Gly Val Phe Thr Val Phe Thr Gly Val Gln
                215                 220                 225

AAT TTC AGC AGG ATC CAT CTG GTG GAC AAA TGG AAC GGA CTC AGC AAG      776
Asn Phe Ser Arg Ile His Leu Val Asp Lys Trp Asn Gly Leu Ser Lys
            230                 235                 240

ATC GAT TAT TGG CAT TCA GAG CAG TGT AAC ATG ATC AAT GGG ACT TCC      824
Ile Asp Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly Thr Ser
        245                 250                 255

GGG CAG ATG TGG GCA CCC TTC ATG ACA CCC GAA TCC TCG CTG GAA TTC      872
Gly Gln Met Trp Ala Pro Phe Met Thr Pro Glu Ser Ser Leu Glu Phe
    260                 265                 270

TTC AGC CCG GAG GCA TGC AGG TCC ATG AAG CTG ACC TAC AAC GAA TCA      920
Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr Asn Glu Ser
275                 280                 285                 290

AGG GTG TTT GAA GGC ATT CCC ACG TAT CGC TTC ACG GCC CCC GAT ACT      968
Arg Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro Asp Thr
                295                 300                 305

CTG TTT GCC AAC GGG TCC GTC TAC CCA CCC AAC GAA GGC TTC TGC CCA     1016
Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe Cys Pro
            310                 315                 320

TGC CGA GAG TCT GGC ATT CAG AAT GTC AGC ACC TGC AGG TTT GGT GCG     1064
Cys Arg Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe Gly Ala
        325                 330                 335

CCT CTG TTT CTC TCC CAC CCC CAC TTT TAC AAC GCC GAC CCT GTG TTG     1112
Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro Val Leu
    340                 345                 350

TCA GAA GCT GTT CTT GGT CTG AAC CCT AAC CCA AAG GAG CAT TCC TTG     1160
Ser Glu Ala Val Leu Gly Leu Asn Pro Asn Pro Lys Glu His Ser Leu
355                 360                 365                 370

TTC CTA GAC ATC CAT CCG GTC ACT GGG ATC CCC ATG AAC TGT TCT GTG     1208
Phe Leu Asp Ile His Pro Val Thr Gly Ile Pro Met Asn Cys Ser Val
                375                 380                 385

AAG ATG CAG CTG AGC CTC TAC ATC AAA TCT GTC AAG GGC ATC GGG CAA     1256
Lys Met Gln Leu Ser Leu Tyr Ile Lys Ser Val Lys Gly Ile Gly Gln
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            390                 395                 400

ACA GGG AAG ATC GAG CCA GTA GTT CTG CCG TTG CTG TGG TTC GAA CAG      1304
Thr Gly Lys Ile Glu Pro Val Val Leu Pro Leu Leu Trp Phe Glu Gln
        405                 410                 415

AGC GGA GCA ATG GGT GGC AAG CCC CTG AGC ACG TTC TAC ACG CAG CTG      1352
Ser Gly Ala Met Gly Gly Lys Pro Leu Ser Thr Phe Tyr Thr Gln Leu
    420                 425                 430

GTG CTG ATG CCC CAG GTT CTT CAC TAC GCG CAG TAT GTG CTG CTG GGG      1400
Val Leu Met Pro Gln Val Leu His Tyr Ala Gln Tyr Val Leu Leu Gly
435                 440                 445                 450

CTT GGA GGC CTC CTG TTG CTG GTG CCC ATC ATC TGC CAA CTG CGC AGC      1448
Leu Gly Gly Leu Leu Leu Leu Val Pro Ile Ile Cys Gln Leu Arg Ser
                455                 460                 465

CAG GAG AAA TGC TTT TTG TTT TGG AGT GGT AGT AAA AAG GGC TCC CAG      1496
Gln Glu Lys Cys Phe Leu Phe Trp Ser Gly Ser Lys Lys Gly Ser Gln
            470                 475                 480

GAT AAG GAG GCC ATT CAG GCC TAC TCT GAG TCC CTG ATG TCA CCA GCT      1544
Asp Lys Glu Ala Ile Gln Ala Tyr Ser Glu Ser Leu Met Ser Pro Ala
        485                 490                 495

GCC AAG GGC ACG GTG CTG CAA GAA GCC AAG CTA TAGGGTCCTG AAGACACTAT    1597
Ala Lys Gly Thr Val Leu Gln Glu Ala Lys Leu
    500                 505

AAGCCCCCCA AACCTGATAG CTTGGTCAGA CCAGCCACCC AGTCCCTACA CCCCGCTTCT    1657

TGAGGACTCT CTCAGCGGAC AGCCCACCAG TGCCATGGCC TGAGCCCCCA GATGTCACAC    1717

CTGTCCGCAC GCACGGCACA TGGATGCCCA CGCATGTGCA AAAACAACTC AGGGACCAGG    1777

GACAGACC                                                             1785
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: misc. feature
(B) LOCATION: 1..509
(D) OTHER INFORMATION: /Function = "Amino acid sequence for the murine Scavenger Receptor Class BI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Gly Gly Ser Ser Arg Ala Arg Trp Val Ala Leu Gly Leu Gly Ala
  1               5                  10                  15

Leu Gly Leu Leu Phe Ala Ala Leu Gly Val Val Met Ile Leu Met Val
            20                  25                  30

Pro Ser Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro
        35                  40                  45

Ser Ser Leu Ser Phe Gly Met Trp Lys Glu Ile Pro Val Pro Phe Tyr
    50                  55                  60

Leu Ser Val Tyr Phe Phe Glu Val Val Asn Pro Asn Glu Val Leu Asn
65                  70                  75                  80

Gly Gln Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu
                85                  90                  95

Phe Arg Gln Lys Val Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser
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                100                 105                 110

Phe Val Glu Asn Arg Ser Leu His Phe Gln Pro Asp Lys Ser His Gly
        115                 120                 125

Ser Glu Ser Asp Tyr Ile Val Leu Pro Asn Ile Leu Val Leu Gly Gly
    130                 135                 140

Ser Ile Leu Met Glu Ser Lys Pro Val Ser Leu Lys Leu Met Met Thr
145                 150                 155                 160

Leu Ala Leu Val Thr Met Gly Gln Arg Ala Phe Met Asn Arg Thr Val
                165                 170                 175

Gly Glu Ile Leu Trp Gly Tyr Asp Asp Pro Phe Val His Phe Leu Asn
            180                 185                 190

Thr Tyr Leu Pro Asp Met Leu Pro Ile Lys Gly Lys Phe Gly Leu Phe
        195                 200                 205

Val Gly Met Asn Asn Ser Asn Ser Gly Val Phe Thr Val Phe Thr Gly
    210                 215                 220

Val Gln Asn Phe Ser Arg Ile His Leu Val Asp Lys Trp Asn Gly Leu
225                 230                 235                 240

Ser Lys Ile Asp Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly
                245                 250                 255

Thr Ser Gly Gln Met Trp Ala Pro Phe Met Thr Pro Glu Ser Ser Leu
            260                 265                 270

Glu Phe Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr Asn
        275                 280                 285

Glu Ser Arg Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro
    290                 295                 300

Asp Thr Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe
305                 310                 315                 320

Cys Pro Cys Arg Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe
                325                 330                 335

Gly Ala Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro
            340                 345                 350

Val Leu Ser Glu Ala Val Leu Gly Leu Asn Pro Asn Pro Lys Glu His
        355                 360                 365

Ser Leu Phe Leu Asp Ile His Pro Val Thr Gly Ile Pro Met Asn Cys
    370                 375                 380

Ser Val Lys Met Gln Leu Ser Leu Tyr Ile Lys Ser Val Lys Gly Ile
385                 390                 395                 400

Gly Gln Thr Gly Lys Ile Glu Pro Val Val Leu Pro Leu Leu Trp Phe
                405                 410                 415

Glu Gln Ser Gly Ala Met Gly Gly Lys Pro Leu Ser Thr Phe Tyr Thr
            420                 425                 430

Gln Leu Val Leu Met Pro Gln Val Leu His Tyr Ala Gln Tyr Val Leu
        435                 440                 445

Leu Gly Leu Gly Gly Leu Leu Leu Leu Val Pro Ile Ile Cys Gln Leu
    450                 455                 460

Arg Ser Gln Glu Lys Cys Phe Leu Phe Trp Ser Gly Ser Lys Lys Gly
465                 470                 475                 480
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Ser Gln Asp Lys Glu Ala Ile Gln Ala Tyr Ser Glu Ser Leu Met Ser
485 490 495

Pro Ala Ala Lys Gly Thr Val Leu Gln Glu Ala Lys Leu
500 505